

# ENTERED



PCT09

## RAW SEQUENCE LISTING

DATE: 07/11/2002

PATENT APPLICATION: US/09/674,377B

TIME: 13:25:17

Input Set : A:\Q61434 Sequence Listing.txt

Output Set: N:\CRF3\07112002\I674377B.raw

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3 <110> APPLICANT: Nakamura, Toshikazu
5 <120> TITLE OF INVENTION: NEOVASCULARIZATION INHIBITORS
7 <130> FILE REFERENCE: Q61434
9 <140> CURRENT APPLICATION NUMBER: 09/674,377B
10 <141> CURRENT FILING DATE: 2000-10-30
12 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01834
13 <151> PRIOR FILING DATE: 1999-04-06
15 <150> PRIOR APPLICATION NUMBER: JP 1998-134681
16 <151> PRIOR FILING DATE: 1998-04-28
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 447
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: MOD_RES
29 <222> LOCATION: (1)..(1)
30 <223> OTHER INFORMATION: pyroglutamate
33 <220> FEATURE:
34 <221> NAME/KEY: CHAIN
35 <222> LOCATION: (1)..(447)
36 <223> OTHER INFORMATION: N-terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)
39 <400> SEQUENCE: 1
41 Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
42 1 5 10 15
45 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
46 20 25 30
49 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
50 35 40 45
53 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
54 50 55 60
57 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
58 65 70 75 80
61 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
62 85 90 95
65 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
66 100 105 110
69 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
70 115 120 125
73 His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn
74 130 135 140
77 Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr

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78 145          150          155          160
81 Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser
82          165          170          175
85 Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met
86          180          185          190
89 Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr
90          195          200          205
93 Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
94          210          215          220
97 Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys
98 225          230          235          240
101 Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr
102          245          250          255
105 Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr
106          260          265          270
109 Glu Cys Ile Gln Gly Gln Gly Glu Tyr Arg Gly Thr Val Asn Thr
110          275          280          285
113 Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His
114          290          295          300
117 Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu
118 305          310          315          320
121 Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr
122          325          330          335
125 Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys
126          340          345          350
129 Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr
130          355          360          365
133 Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp
134          370          375          380
137 Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
138 385          390          395          400
141 Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala
142          405          410          415
145 His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
146          420          425          430
149 Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
150          435          440          445

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153 &lt;210&gt; SEQ ID NO: 2

154 &lt;211&gt; LENGTH: 442

155 &lt;212&gt; TYPE: PRT

156 &lt;213&gt; ORGANISM: Homo sapiens

158 &lt;220&gt; FEATURE:

159 &lt;221&gt; NAME/KEY: VARSPLIC

160 &lt;222&gt; LOCATION: (130)..(131)

161 &lt;223&gt; OTHER INFORMATION: deletion of five amino acids

164 &lt;220&gt; FEATURE:

165 &lt;221&gt; NAME/KEY: CHAIN

166 &lt;222&gt; LOCATION: (1)..(442)

167 <223> OTHER INFORMATION: N-terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)

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170 <220> FEATURE:
171 <221> NAME/KEY: MOD_RES
172 <222> LOCATION: (1)..(1)
173 <223> OTHER INFORMATION: pyroglutamate
176 <400> SEQUENCE: 2
178 Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
179 1 5 10 15
182 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
183 20 25 30
186 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
187 35 40 45
190 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
191 50 55 60
194 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
195 65 70 75 80
198 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
199 85 90 95
202 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
203 100 105 110
206 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
207 115 120 125
210 His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro
211 130 135 140
214 Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val
215 145 150 155 160
218 Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met
219 165 170 175
222 Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser
223 180 185 190
226 Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys
227 195 200 205
230 Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys
231 210 215 220
234 Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro
235 225 230 235 240
238 His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr
239 245 250 255
242 Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly
243 260 265 270
246 Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile
247 275 280 285
250 Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr
251 290 295 300
254 Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn
255 305 310 315 320
258 Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile
259 325 330 335
262 Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly
263 340 345 350

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266 Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser
267      355      360      365
270 Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu
271      370      375      380
274 Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn
275 385      390      395      400
278 Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys
279      405      410      415
282 Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg
283      420      425      430
286 Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
287      435      440

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**VERIFICATION SUMMARY**

DATE: 07/11/2002

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